Household secondary attack rates of SARS-CoV-2 by variant and vaccination status: an updated systematic review and meta-analysis

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Summary: Household secondary attack rates (SARs) were higher for Alpha and Delta variants than previous estimates. SARs were higher to unvaccinated contacts than to partially or fully vaccinated contacts and were higher from unvaccinated index cases than from fully vaccinated index cases.

Abstract

We previously reported a household secondary attack rate (SAR) for SARS-CoV-2 of 18.9% through June 17, 2021. To examine how emerging variants and increased vaccination have affected transmission rates, we searched PubMed from June 18, 2021, through January 7, 2022. Meta-analyses used generalized linear mixed models to obtain SAR estimates and 95%CI, disaggregated by several covariates. SARs were used to estimate vaccine effectiveness based on the transmission probability for susceptibility ($VE_{S,p}$), infectiousness ($VE_{I,p}$), and total vaccine effectiveness ($VE_{T,p}$). Household SAR for 27 studies with midpoints in 2021 was 35.8% (95%CI, 30.6%-41.3%), compared to 15.7% (95%CI, 13.3%-18.4%) for 62 studies with midpoints through April 2020. Household SARs were 38.0% (95%CI, 36.0%-40.0%), 30.8% (95%CI, 23.5%-39.3%), and 22.5% (95%CI, 18.6%-26.8%) for Alpha, Delta, and Beta, respectively. $VE_{I,p}$, $VE_{S,p}$, and $VE_{T,p}$ were 56.6% (95%CI, 28.7%-73.6%), 70.3% (95%CI, 59.3%-78.4%), and 86.8% (95%CI, 76.7%-92.5%) for full vaccination, and 27.5% (95%CI, -6.4%-50.7%), 43.9% (95%CI, 21.8%-59.7%), and 59.9% (95%CI, 34.4%-75.5%) for partial vaccination, respectively. Household contacts exposed to Alpha or Delta are at increased risk of infection compared to the original wild-type strain. Vaccination reduced susceptibility to infection and transmission to others.

Introduction

A previous systematic review and meta-analysis of household transmission of SARS-CoV-2 published through June 17, 2021 reported an overall secondary attack rate (SAR) of 18.9% (95% CI, 16.2%-22.0%) [1]. Emerging variants of concern and increased vaccination have affected transmission rates. Delta (B.1.617.2) became the predominant variant in many parts of the world and Omicron (B.1.1.529) poses additional challenges given its high level of spike mutations and increased potential for transmissibility [2, 3]. Other variants of concern include Alpha (B.1.1.7), Beta (B.1.351), and Gamma (P.1).

Vaccine efficacies against symptomatic disease and death have been demonstrated in randomized controlled trials [4] and vaccine effectiveness has been corroborated in large observational studies in Denmark [5], Israel [6], and the United Kingdom [7]. Household studies can supplement efficacy trials to determine vaccine effectiveness. Vaccine studies based on secondary attack rates (SARs) can be used to estimate the protective effectiveness of a vaccine in vaccinated susceptible contacts compared to unvaccinated susceptible contacts who are exposed to an infected index case ($VE_{S,p}$) [8, 9]. Household studies also enable estimation of vaccine effectiveness in reducing infectiousness ($VE_{I,p}$) by comparing SARs from vaccinated and from unvaccinated index cases to household contacts, which was done for pertussis [10]. Total vaccine effectiveness ($VE_{T,p}$), or the combined effect of direct vaccine protection and indirect vaccine effectiveness, can also be estimated. It is unknown how effective the SARS-CoV-2 vaccines are in reducing susceptibility and infectiousness in the confines of the household where there is prolonged close contact between household members and index cases. Here, we aggregate evidence of household contact tracing studies to evaluate SARs for variants of concern and by index case or contact vaccination status.

Methods

This study followed the Preferred Reporting Items for Systematic Reviews and Meta-analyses (PRISMA) reporting guideline using the same definitions and eligibility criteria as our original study [11]. Our last review identified studies published through June 17, 2018 [1]. Herein, we searched PubMed and reference lists of eligible studies between June 18, 2021, and January 7, 2022, with no restrictions on language, study design, or place of publication. Search terms were: "SARS-CoV-2", "COVID-19", "severe acute respiratory syndrome", "SARS", "SARS-CoV", "coronavirus", "variant", "vaccination", “immunization", "secondary attack rate", "secondary infection rate", "household", "family contacts", "close contacts", "index case", "contact transmission", "contact attack rate", and "family transmission" (S1 Table). Pre-prints were included. Citations were managed in EndNote 20 (Thomson Reuters, Toronto, CA).

Articles with original data that reported at least 2 of the following factors were included: number of infected household contacts, total number of household contacts, and household secondary attack rates. Studies that reported infection prevalence, included populations that overlapped with another included study, and tested contacts using antibody tests only or using antibody tests and another test but did not disaggregate SARs by test were excluded. We first screened studies by titles and abstracts to identify potential studies for inclusion. That reviewer then evaluated full-text articles and selected those that met the inclusion criteria.

For this study, we extracted the following information: first author, location, index case identification period, number of index cases, index case symptom status, household/family contact type, test used to diagnose contacts, universal/symptomatic testing, number of tests per contact, and follow-up duration. We also extracted the number of infected household contacts and total number of household contacts and disaggregated by covariates including variant, index case vaccination status, household contact vaccination status, and vaccine type.

To examine temporal patterns, we assessed household SARs by index case identification period midpoint. We restricted this analysis to laboratory-confirmed infections and SARs from unvaccinated index cases to unvaccinated household contacts to observe how transmission patterns changed

independent of vaccination. Next, we evaluated household SARs by variants that were reported in ≥2 studies regardless of vaccination status and restricted to SARs from unvaccinated index cases to unvaccinated contacts for comparison with SAR estimates from our original analyses of the predominantly wild-type variant [1, 11].

Traditionally, vaccine efficacies for reducing susceptibility and infectiousness are estimated as $VE_{S,p} = 1 - SAR_{01}/SAR_{00}$ and $VE_{I,p} = 1 - SAR_{10}/SAR_{00}$ respectively, where SAR_{ij} is the SAR associated with vaccine status i (1=vaccinated, 0=unvaccinated) for the index case and j for the household contact [8]. The total vaccine effectiveness is defined as $VE_{T,p} = 1 - (1 - VE_{S,p})(1 - VE_{I,p})$. We examined SARs by index case vaccination status (unvaccinated, partially vaccinated, fully vaccinated, all) and household contact vaccination status (unvaccinated, partially vaccinated, fully vaccinated, all). The resultant SARs were used to estimate $VE_{S,p}$, $VE_{I,p}$, and $VE_{T,p}$. We created forest plots of SARs by index case vaccination status to all household contacts regardless of vaccination status and restricted to unvaccinated contacts only. We also created forest plots of SARs by contact vaccination status from all index cases regardless of vaccination status and from unvaccinated index cases only. Furthermore, we evaluated SARs by vaccine type and vaccination status for index cases and/or household contacts if reported in ≥2 studies. Finally, we evaluated SARs by variant and vaccination status for index cases and/or household contacts if reported in ≥2 studies.

Evaluation of Study Quality and Risk of Bias

To assess study quality and risk of bias, we used the same modified version of the Newcastle-Ottawa quality assessment scale used by Fung *et al*. and in our first analysis [11, 12]. Studies received up to 9 points based on participant selection (4 points), study comparability (1 point), and outcome of interest (4 points). Studies were classified as having high (≤3 points), moderate (4-6 points), and low (≥7 points) risk of bias. When at least 10 studies were available, we also used funnel plots and Begg and Mazumdar's rank correlation to evaluate publication bias with significance set at P<0.10 [13].

Statistical Analysis

We used generalized linear mixed-effects models to obtain SAR estimates and 95% CIs. For comparisons across covariate subgroups (variant, index case vaccination status, household contact vaccination status, vaccine type), study was treated as a random effect and the covariate as a fixed effect moderator. For analyses of SARs by index case vaccination status and contact vaccination status, comparisons between subgroups (e.g., fully vaccinated versus unvaccinated index cases) were restricted to pairwise analyses (studies in which SARs were reported from both fully vaccinated and unvaccinated index cases). For vaccine effectiveness measures, we also used generalized linear mixed models to obtain the logit of the SAR and corresponding sampling variances, which were back-transformed to obtain VE summary estimates and 95%CIs. Heterogeneity was measured using the I^2 statistic, with thresholds of 25%, 50%, and 75% indicating low, moderate, and high heterogeneity, respectively. All analyses were performed using the metafor package in R software, version 4.1.2 (R Foundation for Statistical Computing) [14, 15]. Statistical significance was set at a 2-tailed P-value$\leq$0.05.

Results

We identified 1,291 records (1,281 from PubMed and 10 from reference lists of eligible articles) published between June 18, 2021 and January 7, 2022 (S1 Figure). Forty-eight new studies [16-64] were included in this review (S2 Table), 4 of which were preprints in our previous review that were subsequently published [53-55, 64].

Forty-nine new studies[16-64] were combined with 77 studies from our previous review [1] for our analysis of household SAR by study period (5 studies were excluded that did not include laboratory-confirmed infections and 1 that included only asymptomatic index cases), resulting in 126 total studies representing 1,437,696 contacts from 35 countries (see S3 Table for references). Figure 1 demonstrates large heterogeneity in SAR over time but estimates with midpoints after July 2020 are generally higher than the earliest estimates. The household SAR for 27 studies with midpoints in 2021 was 35.8% (95%CI,

30.6%-41.3%), whereas the household SAR for 62 studies with midpoints through April 2020 was 15.7% (95%CI, 13.3%-18.4%). Begg and Mazumdar's rank correlation was statistically significant for studies in 2021 (P=0.001), but not studies through April 2020 (S2 Figure). Excluding one study in 2021 [54] that had a relatively low SAR improved the funnel plot symmetry and resulted in a SAR of 33.9% (95%CI, 29.4%-38.7%) for studies with midpoints in 2021. When restricting to unvaccinated contacts only, the household SAR for studies with midpoints in 2021 was 35.4% (95%CI, 30.0%-41.2%).

Eight new studies [23, 28, 31, 39, 50, 52, 55, 56] were combined with 1 study [65] from our previous review for our analysis of Alpha variant. Figure 2 summarizes results from these 9 studies as well as 12 [23, 25, 29, 32, 41, 43, 48, 52, 56, 61-63] and 3 [20, 23, 56] new studies reporting household SARs for Delta and Beta variants, respectively. Estimated mean household SAR for Alpha was 38.0% (95%CI, 36.0%-40.0%), Delta was 30.8% (95%CI, 23.5%-39.3%), and Beta was 22.5% (95%CI, 18.6%-26.8%) (Figure 2). SARs between Alpha/Delta and Delta/Beta were not significantly different, but Alpha was significantly higher than Beta (P<0.001). High heterogeneity was found among studies for Delta (98.0%), and low for Alpha (16.7%) and Beta (2.6%). Begg correlation was not significant for studies of Delta (S3 Figure). SARs did not significantly change for Alpha (37.8%, 95%CI, 35.7%-39.9%) (5 studies) [23, 28, 31, 50, 55] or Delta (27.0%, 95%CI, 18.5%-37.4%) (7 studies) [23, 29, 32, 43, 48, 61, 62] when restricting to studies with low risk of bias (S4 Table). Restricting to unvaccinated contacts only, mean estimated SAR for Delta was 34.9% (95%CI, 26.7%-44.1%) (S4 Figure).

Eight studies [24, 26, 34, 39, 43, 48, 54, 62] reported SARs by vaccination status of the index case to all household contacts regardless of vaccination status, seven of which were at low risk of bias and one was moderate (Figure 3). Overall estimated mean SAR was 26.6% (95%CI, 18.7%-36.4%) from unvaccinated (8 studies) [24, 26, 34, 39, 43, 48, 54, 62], 16.2% (95%CI, 8.3%-29.4%) from partially vaccinated (5 studies) [24, 43, 48, 54, 62], and 14.4% (95% CI: 10.5%-19.4%) from fully vaccinated (7 studies) [24, 26, 34, 39, 43, 48, 62] index cases to household contacts. For 7 paired studies [24, 26, 34, 39, 43, 48, 62], estimated mean SAR from unvaccinated index cases (29.9%; 95%CI, 23.0%-37.7%) was significantly higher than from fully vaccinated index cases (P<0.001). For 5 paired studies [24, 43, 48,

54, 62], SARs were not significantly different from unvaccinated index cases (19.7%; 95%CI, 13.9%-27.3%) than from partially vaccinated index cases. Three studies included only Delta infections [43, 48, 62]. Restricting to those 3 studies, we found no significant difference in SAR by index case vaccination status to all contacts regardless of vaccination status. Excluding those 3 studies, the estimated mean SAR was significantly higher from unvaccinated index cases (36.3%; 95%CI, 31.3%-41.6%) than from fully vaccinated index cases (10.7%; 95%CI, 9.0%-12.8%) (P<0.001) (4 paired studies) [24, 26, 34, 39], but not from partially vaccinated index cases (2 paired studies) [24, 54]. Restricting to unvaccinated household contacts, SARs were also significantly higher from unvaccinated index cases (30.9%, 95%CI, 23.9%-38.8%) than from fully vaccinated index cases (12.0%, 95%CI, 10.0%-14.2%) (P<0.001) (4 paired studies) [24, 26, 48, 62], but not from partially vaccinated index cases (3 paired studies) [24, 54, 62] (S5 Figure). SARs were generally lower from fully vaccinated index cases regardless of contact vaccination status (S6 Figure). Direct comparison of these studies is compromised, however, because of differences between studies in terms of vaccine types, definition of vaccination status (e.g., time elapsed since vaccination or dosage) (S5 Table), vaccination coverage among contacts, characteristics of the study population, duration of follow-up, diagnostic procedures and tools, location, magnitude of the pandemic, and circulating variants.

Figure 4 summarizes 9 studies [24, 26, 34, 38, 43, 48, 56, 62, 63] reporting household SARs by contact vaccination status regardless of index case vaccination status, eight of which were at low risk of bias and two were moderate. Overall estimated mean SAR was 33.8% (95%CI, 28.0%-40.2%) to unvaccinated contacts (9 studies) [24, 26, 34, 38, 43, 48, 56, 62, 63], 23.7% (95%CI, 19.1%-28.9%) to partially vaccinated contacts (6 studies) [24, 38, 43, 48, 56, 63], and 14.1% (95%CI, 10.6%-18.6%) to fully vaccinated contacts (9 studies) [24, 26, 34, 38, 43, 48, 56, 62, 63]. In the 9 paired studies, estimated mean household SARs were significantly higher to unvaccinated contacts than to fully vaccinated contacts (P<0.001). For 6 paired studies [24, 38, 43, 48, 56, 63], SARs were significantly higher to unvaccinated contacts (33.1%, 95%CI, 27.8%-38.8%) than to partially vaccinated contacts (P=0.020), but SARs were not significantly different to partially vaccinated contacts than to fully vaccinated contacts

(16.6%, 95%CI, 11.9%-22.9%). SARs were consistent when restricting to only unvaccinated index cases (4 studies [24, 26, 48, 62]) (S7 Figure). When restricting to 4 studies [43, 48, 62, 63] that targeted Delta, SARs were also significantly higher to unvaccinated contacts (24.4%, 95%CI, 19.3%-30.4%) than to fully vaccinated contacts (14.3%, 95%CI, 9.3%-21.3%) (P=0.027). We also estimated vaccine effectiveness based on the SARs (Table 1).

Next, we examined SARs by vaccine type and index case vaccination status regardless of vaccination status of household contacts. SARs were included in 2 studies [26, 39] for BNT162b2 and the mean estimated SAR from fully vaccinated index cases was 8.3% (95%CI, 5.6%-12.1%) compared to 35.9% from unvaccinated index cases (95%CI, 34.1%-37.6%) (S8 Figure).

We also examined SARs by vaccine type and contact vaccination status regardless of index case vaccination status (3 studies [24, 38, 56]). Mean estimated SAR to household contacts fully vaccinated with Ad26.COV2.S (1 dose) (42.7%, 95% CI: 13.6%-77.9%) (P=0.005) or BNT162b2 (15.8%, 95%CI, 15.0%-16.7%) (P<0.001) was significantly higher than to contacts fully vaccinated with mRNA-1273 (2 doses) (6.2%, 95% CI: 2.8%-13.0%) (S9 Figure). Additionally, mean estimated SAR was higher to contacts partially vaccinated with ChAdOx1-S (29.5%, 95% CI: 24.0%-35.7%) than contacts partially vaccinated with mRNA-1273 (17.5%, 95%CI, 13.7%-22.3%) (P=0.008). There was no significant difference in SAR to contacts fully vaccinated for ChAdOx1-S and BNT162b2, Ad26.COV2.S, or mRNA-1273; or to contacts partially vaccinated for BNT162b2 and mRNA-1273or ChAdOx1-S.

Discussion

We aggregated household studies to examine how variants of concern and vaccination affected household transmission rates of SARS-CoV-2. Household SARs from fully vaccinated index cases were lower than from unvaccinated index cases. Fully and partially vaccinated household contacts were less susceptible to SARS-CoV-2 infection than unvaccinated contacts. SARs for Delta and Alpha were significantly higher than estimates for the original wild-type variant.

Several individual studies included in this analysis reported that full vaccination of index cases significantly reduced the risk of transmission to household contacts [24, 34]. Conversely, other studies included in this analysis reported that vaccination status of the index case was not associated with household contact infection [43, 48]. A meta-analysis allows us to aggregate all the evidence of index case vaccination status from multiple studies and control for differences between the studies. We found lower transmission to household contacts from fully vaccinated index cases than from unvaccinated index cases, but not from partially vaccinated index cases. An observational cohort study from England which included contacts outside the household also reported that two doses of BNT162b2 or ChAdOx1 reduced onward transmission of Delta, but by less than Alpha, and the impact of vaccination against onward transmission waned over time [66]. Our estimate for $VE_{I,p}$ of 56.6% was within the 41%-79% range reported for VE_I from a modeling study that used household data from Israel before Delta became widespread [67]. Potential mechanisms for reduced infectiousness following vaccination include decreases in the respiratory tract viral load and severity of symptoms [68].

Fully vaccinated and partially vaccinated contacts had significantly lower SARs than unvaccinated contacts. Other observational studies demonstrated reduced susceptibility to infection among high risk or household contacts vaccinated with BNT162b2 or ChAdOx1 in Scotland [69], BNT162b2 in Sweden [70], and BNT162b2 or mRNA-1273 in Belgium [71]. Studies have reported that full vaccination with mRNA vaccines or ChAdOx1 effectively prevent infection against the original wild-type, Alpha, and Beta variants, but are less protective against infection for Delta [72, 73]. Our estimates of $VE_{S,p}$ (70.3%, 95%CI, 59.3%-78.4%) and $VE_{T,p}$ (86.8%, 95%CI, 76.7%-92.5%) were slightly lower than the age-adjusted VE_S (80.5%, 95%CI, 78.9%-82.1%) and VE_T (88.5%, 95%CI, 82.3%-94.8%) reported by *Prunas et al* [67]. Myriad factors preclude our ability to make direct comparisons of vaccine effectiveness across studies including differences in the study population (e.g., age, comorbidities, serostatus), viral characteristics, vaccine type, time period defining vaccination status, intensity of the epidemic, community behavior, and use of nonpharmaceutical interventions (masks, social distancing)

238 [74]. For example, in this analysis *Singanayagam et al.* [48] included households of any size with
239 contacts ≥5 years, whereas *Gazit et al.* [26] restricted to households with only one contact other than the
240 index case. Moreover, *Ng et al.* in Singapore reported that all identified close contacts were placed under
241 a legally-binding quarantine for 14 days during which they were not allowed to leave their homes [43],
242 whereas contacts in other studies may have had a higher risk of infection outside the household.
243 With the addition of 49 studies since our last review [1], we observed higher SARs in 2021 than
244 earlier in the pandemic. This pattern may be attributed in part to the emergence of more contagious
245 variants. SAR estimates for Alpha (38.0%) and Delta (30.8%) variants were both higher than the overall
246 SAR previously reported (18.9%) for study periods earlier in the pandemic when the wild-type variant
247 was prevalent [1]. Public Health England (PHE), which tracks SARs for variants of concern and variants
248 of interest regardless of vaccination status for index cases and household contacts, found SARs similar for
249 Alpha (10.2%, 95%CI, 10.1%-10.3%) and Delta (10.4%, 95%CI, 10.4%-10.5%) variants [75]. They note,
250 however, that direct comparisons between variants are not valid as vaccination levels and social
251 restrictions in England have varied over this period. Similarly, SARs for Delta and Alpha were not
252 significantly different in this study even when restricting to unvaccinated contacts only, which may be
253 partially attributed to an increase in population immunity consequent to infection. A prospective cohort
254 study [22] and case-control study [76] in England demonstrated increased household transmission for
255 Delta compared to Alpha. Increased transmissibility may be attributed to higher viral loads, shorter
256 incubation periods, and mutations in the spike glycoprotein of the virus, which may confer immune
257 escape potential [77]. Delta infections produced more viral RNA copies per mL than Alpha infections
258 [78], its *in vitro* replication rate is higher than Alpha [79], and its spike protein binds more efficiently to
259 the host cell entry receptor ACE2 protein [80].
260 There was large heterogeneity in SARs over time which may be attributed to variations in study
261 methods, environmental factors, and contact patterns. Comparisons of SARs by vaccination status
262 between studies were also hindered by differences between studies and there were few studies
263 disaggregating SARs by both vaccination status of the index cases and contacts. The studies included in

this review are from contact tracing investigations which are more likely to identify symptomatic index cases than asymptomatic individuals, which could inflate the crude SAR. This may also underestimate the reduction in transmission from vaccination for people infected with Delta [81]. Our analyses by vaccine type and Beta variant were limited to three studies. There was insufficient data to determine vaccine effectiveness for specific subgroups (e.g., by age group) and whether that varied by variant.

Household contacts exposed to Delta or Alpha variants are at increased risk of infection compared to the original wild-type variant from Wuhan. Vaccination was demonstrated to reduce susceptibility to infection and infectiousness. The household remains an important venue of transmission for SARS-CoV-2. Other public health measures such as hygiene, increased testing, isolation, and improved ventilation may help limit its spread. Preliminary analyses from PHE demonstrate increased odds of household transmission from Omicron index cases than from Delta index cases, adjusting for index case vaccination status and other factors [82]. A study from Denmark reported higher transmission rates for Omicron than Delta for fully vaccinated individuals but not unvaccinated individuals [61]. The transmissibility and virulence of Omicron is only now being elucidated and other variants are likely to emerge.

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Figure Legends

Figure 1. Household secondary attack rates over time (by study midpoint), 126 studies (unvaccinated index cases, unvaccinated contacts). Restricted to laboratory-confirmed results only. The blue line is a loess smoothing line and bands are 95% confidence intervals. Bicolored points represent studies with 2 predominant variants.

Figure 2. Household secondary attack rates for Alpha (B.1.1.7), Delta (B.1.617.2), and Beta (B.1.351) variants.

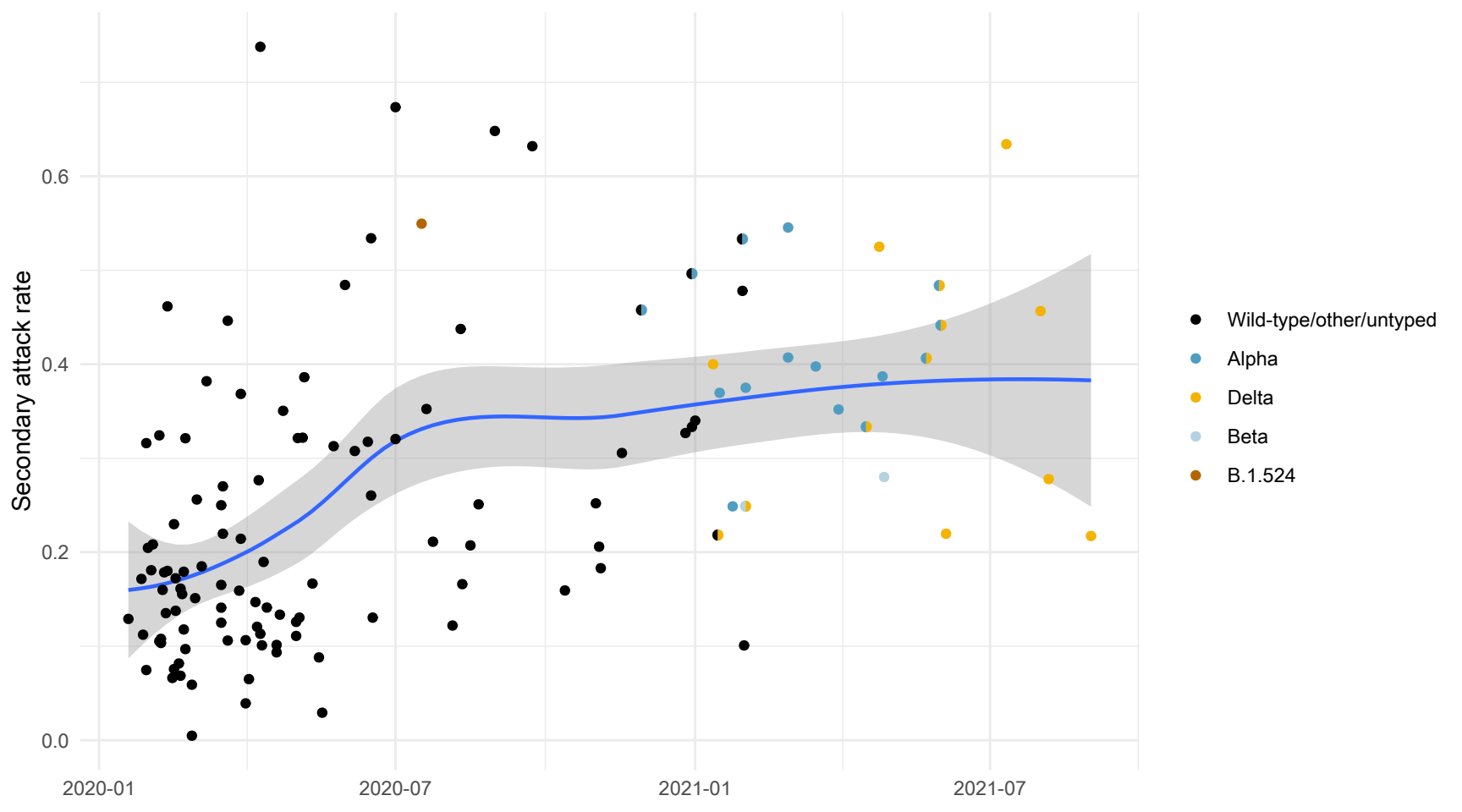
Figure 3. Household secondary attack rates by index case vaccination status. All contacts are included regardless of vaccination status. *For Harris *et al.*, most of the vaccinated index cases (93%) had received only the first dose of vaccine and secondary attack rates were not disaggregated by dose.

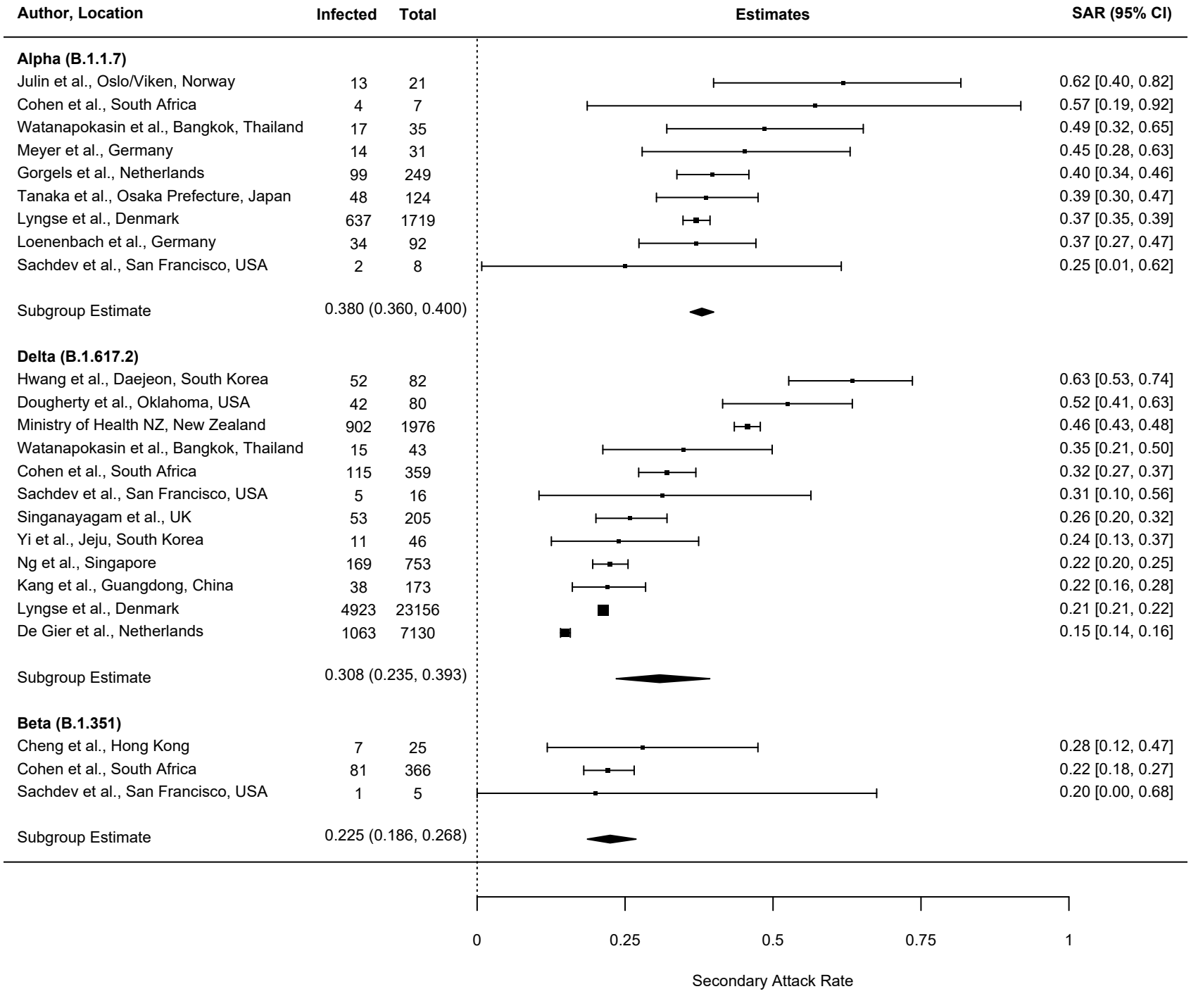
Figure 4. Household secondary attack rates by contact vaccination status. All index cases are included regardless of vaccination status.

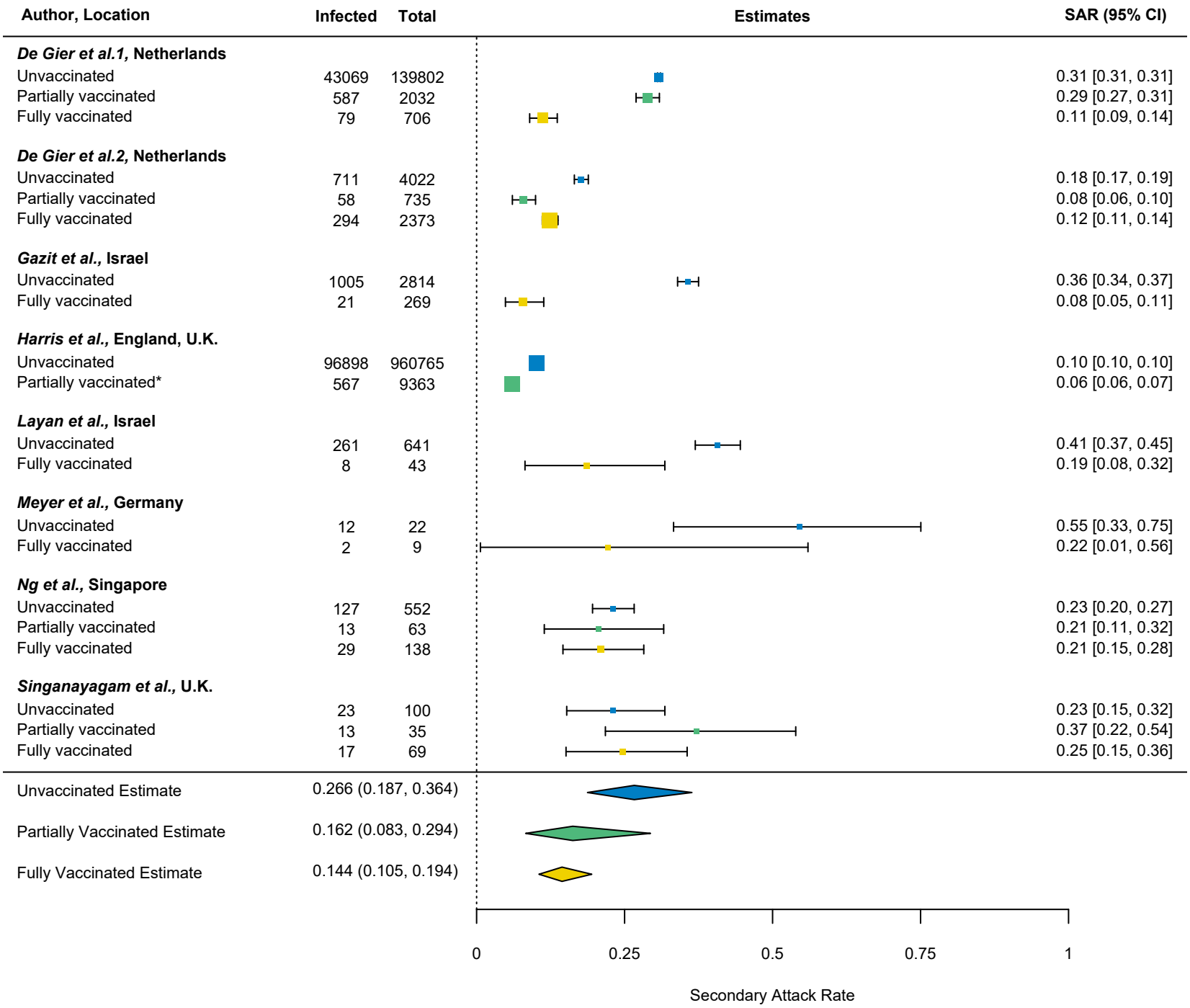
Table 1. Estimated vaccine effectiveness (95%CI) estimates from household secondary attack rates.

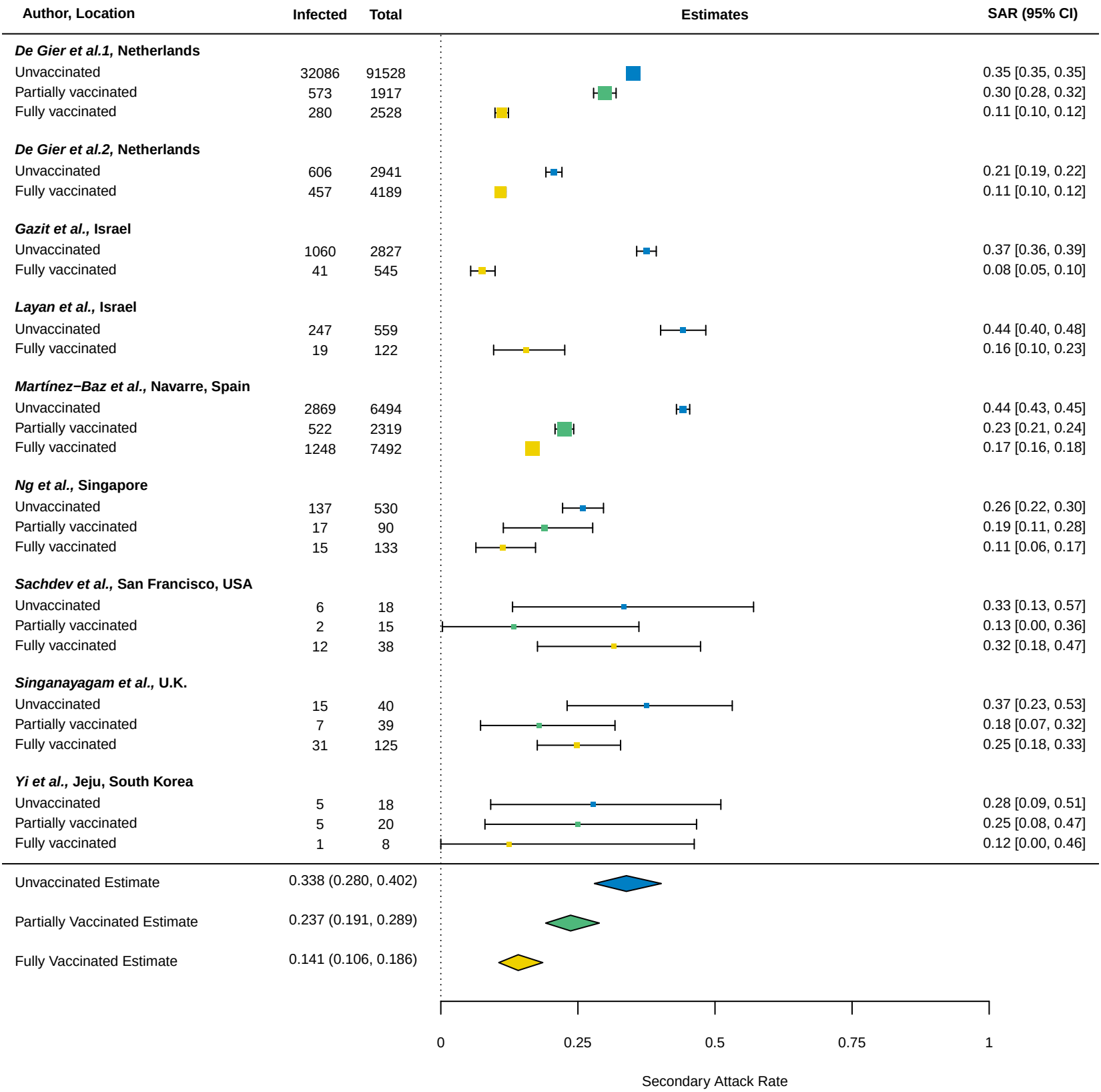
Vaccine effectiveness	Full Vaccination	Partial Vaccination
$VE_{I,p}$	56.6% (28.7%-73.6%)	27.5% (-6.4%-50.7%)
$VE_{S,p}$	70.3% (59.3%-78.4%)	43.9% (21.8%-59.7%)
$VE_{T,p}$	86.8% (76.7%-92.5%)	59.9% (34.4%-75.5%)

$VE_{I,p}$: vaccine effectiveness for infectiousness based on the transmission probability p; $VE_{S,p}$: vaccine effectiveness for susceptibility; $VE_{T,p}$: total vaccine effectiveness


Secondary attack rate
0.0
0.2
0.4
0.6
2020-01
2020-07
2021-01
2021-07
Wild-type/other/untyped
Alpha
Delta
Beta
B.1.524


Author, Location
Infected
Total
Estimates
SAR (95% CI)
Alpha (B.1.1.7)
Julin et al., Oslo/Viken, Norway 13 21 0.62 [0.40, 0.82]
Cohen et al., South Africa 4 7 0.57 [0.19, 0.92]
Watanapokasin et al., Bangkok, Thailand 17 35 0.49 [0.32, 0.65]
Meyer et al., Germany 14 31 0.45 [0.28, 0.63]
Gorgels et al., Netherlands 99 249 0.40 [0.34, 0.46]
Tanaka et al., Osaka Prefecture, Japan 48 124 0.39 [0.30, 0.47]
Lyngse et al., Denmark 637 1719 0.37 [0.35, 0.39]
Loenenbach et al., Germany 34 92 0.37 [0.27, 0.47]
Sachdev et al., San Francisco, USA 2 8 0.25 [0.01, 0.62]
Subgroup Estimate 0.380 (0.360, 0.400)
Delta (B.1.617.2)
Hwang et al., Daejeon, South Korea 52 82 0.63 [0.53, 0.74]
Dougherty et al., Oklahoma, USA 42 80 0.52 [0.41, 0.63]
Ministry of Health NZ, New Zealand 902 1976 0.46 [0.43, 0.48]
Watanapokasin et al., Bangkok, Thailand 15 43 0.35 [0.21, 0.50]
Cohen et al., South Africa 115 359 0.32 [0.27, 0.37]
Sachdev et al., San Francisco, USA 5 16 0.31 [0.10, 0.56]
Singanayagam et al., UK 53 205 0.26 [0.20, 0.32]
Yi et al., Jeju, South Korea 11 46 0.24 [0.13, 0.37]
Ng et al., Singapore 169 753 0.22 [0.20, 0.25]
Kang et al., Guangdong, China 38 173 0.22 [0.16, 0.28]
Lyngse et al., Denmark 4923 23156 0.21 [0.21, 0.22]
De Gier et al., Netherlands 1063 7130 0.15 [0.14, 0.16]
Subgroup Estimate 0.308 (0.235, 0.393)
Beta (B.1.351)
Cheng et al., Hong Kong 7 25 0.28 [0.12, 0.47]
Cohen et al., South Africa 81 366 0.22 [0.18, 0.27]
Sachdev et al., San Francisco, USA 1 5 0.20 [0.00, 0.68]
Subgroup Estimate 0.225 (0.186, 0.268)
0
0.25
0.5
0.75
1
Secondary Attack Rate


Author, Location
Infected
Total
Estimates
SAR (95% CI)
De Gier et al.1, Netherlands
Unvaccinated 43069 139802 0.31 [0.31, 0.31]
Partially vaccinated 587 2032 0.29 [0.27, 0.31]
Fully vaccinated 79 706 0.11 [0.09, 0.14]
De Gier et al.2, Netherlands
Unvaccinated 711 4022 0.18 [0.17, 0.19]
Partially vaccinated 58 735 0.08 [0.06, 0.10]
Fully vaccinated 294 2373 0.12 [0.11, 0.14]
Gazit et al., Israel
Unvaccinated 1005 2814 0.36 [0.34, 0.37]
Fully vaccinated 21 269 0.08 [0.05, 0.11]
Harris et al., England, U.K.
Unvaccinated 96898 960765 0.10 [0.10, 0.10]
Partially vaccinated* 567 9363 0.06 [0.06, 0.07]
Layan et al., Israel
Unvaccinated 261 641 0.41 [0.37, 0.45]
Fully vaccinated 8 43 0.19 [0.08, 0.32]
Meyer et al., Germany
Unvaccinated 12 22 0.55 [0.33, 0.75]
Fully vaccinated 2 9 0.22 [0.01, 0.56]
Ng et al., Singapore
Unvaccinated 127 552 0.23 [0.20, 0.27]
Partially vaccinated 13 63 0.21 [0.11, 0.32]
Fully vaccinated 29 138 0.21 [0.15, 0.28]
Singanayagam et al., U.K.
Unvaccinated 23 100 0.23 [0.15, 0.32]
Partially vaccinated 13 35 0.37 [0.22, 0.54]
Fully vaccinated 17 69 0.25 [0.15, 0.36]
Unvaccinated Estimate 0.266 (0.187, 0.364)
Partially Vaccinated Estimate 0.162 (0.083, 0.294)
Fully Vaccinated Estimate 0.144 (0.105, 0.194)
0
0.25
0.5
0.75
1
Secondary Attack Rate


Author, Location
Infected
Total
Estimates
SAR (95% CI)
De Gier et al.1, Netherlands
Unvaccinated 32086 91528 0.35 [0.35, 0.35]
Partially vaccinated 573 1917 0.30 [0.28, 0.32]
Fully vaccinated 280 2528 0.11 [0.10, 0.12]
De Gier et al.2, Netherlands
Unvaccinated 606 2941 0.21 [0.19, 0.22]
Fully vaccinated 457 4189 0.11 [0.10, 0.12]
Gazit et al., Israel
Unvaccinated 1060 2827 0.37 [0.36, 0.39]
Fully vaccinated 41 545 0.08 [0.05, 0.10]
Layan et al., Israel
Unvaccinated 247 559 0.44 [0.40, 0.48]
Fully vaccinated 19 122 0.16 [0.10, 0.23]
Martínez−Baz et al., Navarre, Spain
Unvaccinated 2869 6494 0.44 [0.43, 0.45]
Partially vaccinated 522 2319 0.23 [0.21, 0.24]
Fully vaccinated 1248 7492 0.17 [0.16, 0.18]
Ng et al., Singapore
Unvaccinated 137 530 0.26 [0.22, 0.30]
Partially vaccinated 17 90 0.19 [0.11, 0.28]
Fully vaccinated 15 133 0.11 [0.06, 0.17]
Sachdev et al., San Francisco, USA
Unvaccinated 6 18 0.33 [0.13, 0.57]
Partially vaccinated 2 15 0.13 [0.00, 0.36]
Fully vaccinated 12 38 0.32 [0.18, 0.47]
Singanayagam et al., U.K.
Unvaccinated 15 40 0.37 [0.23, 0.53]
Partially vaccinated 7 39 0.18 [0.07, 0.32]
Fully vaccinated 31 125 0.25 [0.18, 0.33]
Yi et al., Jeju, South Korea
Unvaccinated 5 18 0.28 [0.09, 0.51]
Partially vaccinated 5 20 0.25 [0.08, 0.47]
Fully vaccinated 1 8 0.12 [0.00, 0.46]
Unvaccinated Estimate 0.338 (0.280, 0.402)
Partially Vaccinated Estimate 0.237 (0.191, 0.289)
Fully Vaccinated Estimate 0.141 (0.106, 0.186)
0
0.25
0.5
0.75
1
Secondary Attack Rate